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(without alignments)
547.808 Million cell updates/sec
                                                                                                                                                                                                                                              738
1 STAPTRSKTPAQGLARKLHF......PTERPRAPARSASRPRRPVE 143
                                                                                                                              May 21, 2003, 17:13:44 ; Search time 34.7838 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                              908470
GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                               908470 seqs, 133250620 residues
                                                                                                                                                                                                                       US-09-522-278B-12_COPY_159_301
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Maximum Match 100%
Listing first 45 summaries
                                                                                      OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* DAT: 'qcadata/qeneseq/qeneseqp-emb1/AA1994.DAT /SIDS2/qcqdata/geneseq/geneseqp-embl/AA1989 /qcqdata/qeneseq/qeneseqp-embl/AA1998 /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000 /SIDS2/qcqdata/qeneseq/qeneseqp-emb1/AA1984. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985./SIDS2/gcgdata/geneseq/geneseqp-embl/AA1986. gcgdata/geneseq/geneseqp-embl/AA1995 /gcgdata/geneseq/geneseqp-embl/AA1980. /SIDS2/gcgdata/geneseq/genesegp-emb1/AA1987. /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1988. /SIDS2/gcgdata/geneseg/genesegp-embl/AA199 qcqdata/qeneseq/qeneseqp-emb1/AA199 /SIDS2/gcgdata/geneseg/genesegp-embl 'gcgdata/geneseg/genesegp /SIDS2/gcgdata/geneseg/genesegp /SIDS2 SIDS2 /SIDS2, /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Herpes simplex vir	Herpes simplex vir	HSV-1 tequment pro	HIV-1 VP22 polypep	HSV-1 V22 cellular	HSV-1 VP22 peptide	HSV-1 VP22 protein	VP22 protein fragm	Herpes simplex vir	HSV-1 VP22 protein
	ID		AAY42292	AAY27404	AAW95099	AAY83261	AAY79877	AAB60910	AAB86329	AAG64275	ABB05524
	DB	19	20	20	20	21	21	22	22	22	23
	Query re Match Length DB I	301	301	301	301	301	301	301	301	301	301
P	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	738	738	738	738	738	738	738	738	738	738
	Result No.	1	7	m	4	S	9	7	80	o	10

PcDNA3-VP22/E7 fus	Delta VP22Cre-Stre	VP22-Cre fusion pr	VP22CreStrepTag fu	VP22-Flpe fusion p	HSV-1 VP22 polypep	HSV-2 strain SB5 C	HSV-2 VP22 protein	Herpes simplex vir	₽.	c	Herpes simplex vir		ಌ	Amino acid sequenc	herp	'n		HIV-1 VP22 polypep			VP22	VP22	HSV-1 VP22 protein	Canine herpesvirus	Canine herpes viru	Canine herpes viru	Herpes simplex vir	Membrane transport	Herpes simplex-1 v		HSV truncated tegu	HSV truncated		HSV truncated tegu ~
35	70	266	73	267	74	14	55	95	30	89	33			62	29	36	93	00	75	62	178	11	25	03	63	20	.95	0	47	54	98	- 25	101	200
AAU772	AAE0527	10	AAE0527	AAE052	AAY965	AAW7221	AAW6775	AAW4719	AAB8633	AAW7206	AAY7833	AAE2317	AAR6346	AAB076	AAU1136	AAU772	AAR65493	AAW951	AAY96575	AAY832	AAY7987	AAB609	ABB05525	AAW230	AAW726	AAB513	AAM481	AAE122	AAU783	AAU783	AAW471	AAW471	AAW4720	AAW472
23	22	22	22	22	21	19	20	19	22	19	21	23	15	21	23	23	16	20	21	21	21	22	23	18	19	22	23	22	23	23	19	19	19	19
418		667	683	747	297	302	306	144	267	117	246	246	257	258	258	249	249	37	37	37	37	37	37	139	139	139	34	34.	34	32	50	50	20	20
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100	100.	100	100	100	66	80	80	77	77	63	56	26	29	28	28	25	24	24	24	24	24	24	. 24			23	22	22	22				14	14
738	738	738	738	738	732	96	596.5	569	569	471	14	4	12	210	210	189	184	179	179	179	179	179	179	72	172.5	7	169	166	164	164	117	108	106	103
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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New antiviral agent disrupting binding of VP22 to VP16 or gB -useful for treating infections caused by herpes simplex, e.g. cold sores and chicken-pox
                                                                                                                                                                                                                                              HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore; genital herpes; chickenpox; shingles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hope RG, McGeoch DJ, McLaughlan J, Rixon HWM;
                                                                                                                                                                                                    Herpes simplex virus tegument protein VP22.
                                               AAW47194 standard; Protein; 301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-GB02036.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96GB-0015726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MEDI-) MEDICAL RES COUNCIL.
                                                                                                                                             03-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                               Herpes simplex virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-130696/12.
N-PSDB; AAV17085.
                                                                                                                                                                                                                                                                                                                                                                            WO9804708-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                           05-FEB-1998.
                                                                                              AAW47194;
RESULT 1
                          AAW47194
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Up22 tegument protein, which is involved in transcellular localisation. VP22 can be fused to cytochrome P450 reductase (P450R) carbustuses such as anchorless P450R (AAY4228B) or For fragment carbustuses such as anchorless P450R (AAY4228B) or For fragment carbustuses anchorless P450R (AAY4228B). This enables the fusion protein to be delivered to neighbouring cells where it is then transported to the nucleus. Many carbustases of action are in the nucleus, rather than the cytoplasm, where P450R normally functions. P450R or its derivatives can be used to activate products to their active form via reduction. Administration of a product is useful where the active form via reduction. Administration of a carbon or where the active drug as cytochoxic, e.g., reaches its site of action or where the active drug activators allows a reduction in dose of the producy, and thus of systemic side-effects. P450R derivative fusion proteins, or vectors that express them, are specifically used to treat tumours, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g., with hypoxial ischaemia or hyposlycemia, or to deliver antibiotics, antiviral agents, analgesics, anaesthetics, anti-inflammatorles, anti-inflammatorles, anti-inflammatorles, anti-inflammatorles, anti-inflammatorles, anti-inflammatorles,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "the corresponding DNA sequence for this region is possibly missing; there are only 4 nucleotide basepairs indicated as encoding for this entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prodrug; localization domain; tumor-selective antibody; cytochrome P450; prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 STAPTRSKTPAGGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rheumatoid arthritis; hypoxla; ischemia; hypoglycemia; HSV; VP22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 738; DB 20;
100.0%; Pred. No. 7.4e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
251..267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY27404 standard; Protein; 301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 ASRPTERPRAPARSASRPRRPVE 301
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98GB-0018103.
99GB-0002081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSV-1 tegument protein VP22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB00672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tegument protein
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19-AUG-1998;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9945126-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY27404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY27404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
251..267
/note= "Corresponding DNA sequence appears to be absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                   QLWDMSRPRIDEDLNELLGITIIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                            1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors -
                                                                                         tegument protein vP22. VP22 was used in the preparation of a novel antiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, gential herpes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Griffiths L;
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                                                                                                                                                                                                                                                                     Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herpes simplex virus type 1 (HSV-1) VP22 tegument protein.
                                                                                                                                                                                                                                                                                                                   Indels
                                                                         The present sequence is the herpes simplex virus (HSV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patterson AV, Kingsman SM, Kan O,
                                                                                                                                                                                                                                                                   100.0%; Score 738; DB 19;
100.0%; Pred. No. 7.4e-76;
ive 0; Mismatches 0;
                         Pages 49-50; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY42292 standard; Protein; 301 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ASRPTERPRAPARSASRPRRPVE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Herpes simplex virus type 1. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99GB-0002081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Fig 3; 187pp;
                                                                                                                                                                                     chickenpox and shingles.
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N-PSDB; AAZ19784.
                                                                                                                                                                                                                            301 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-MAR-1998;
19-AUG-1998;
29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09945127-A2
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                             Example;
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                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                      159
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ID AAY
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Mitrophanous K; Stratford IJ,

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The invention relates to novel inhibitors of cyclin-dependent kinases (CDKs), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (i) first gene construct comprising a sequence encoding an inhibitory polypeptide containing at last one CDK-binding motif for binding and inhibiting activity of a comprise to a transcription regulator functional in eukaryotic cells; (ii) second gene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition that promotes endothelialisation, and (iii) a gene delivery composition or collect acids encoding a fusion protein (FP) containing: (i) a therapeutic polypeptide sequence (TP) from an intracellular protein that a real-ular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of transcellular polypeptide sequence (TCP) that promotes transcytosis of transcellular polypeptide sequence (TCP) that promotes transcytosis of transcellular of detailed uses of the recombinant transfection system. The CXI polypeptides are engineered to include any of the peptides shown in AMW95097-100 encoded by the DNA sequences AAX26225-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems.
                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 738; DB 20; 100.0%; Pred. No. 7.4e-76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 26-27; 88pp; English.
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                                                                                                                                                                                                                                                                                              Lamphere L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 ASRPTERPRAPARSASRPRRPVE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibrosis and neurodegeneration
                                                                                                                                 98WO-US15759
                                                                                                                                                                                   97US-0902572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                           Gyuris J,
                                                                                                                                                                                                                                                                                                                                              WPI; 1999-153770/13
                                                                                                                                                                                                                                         (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AA;
                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAX26227
                         W09906540-A2
                                                                                                                                 29-JUL-1998;
                                                                                                                                                                                   29-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 143;
                                                                                                                                                                                                                                                                                           Beach DH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY83261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a localization domain (LD) other than a timer-selective antibody) and a produg activating domain (PAD); (ii) at least one nucleic acid encoding a cytochrome P450 and under control of at least one nucleic acid encoding a cytochrome P450 and under control of elements as in (ii); a modified hematopoietic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and under control of elements as in (ii). The produg activating agent or vectors that express them, are specifically used to treat tumors, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g. cerebral malaria, rheumatoid arthritis, or conditions associated with hyposiy-cemia or ischemia, or to deliver antibiotics, antiviral agents and diagnostic agents. LD optimize activity of PAD, e.g. by delivering it to selected locations or by delivering it to neighboring cells (bystander effect), and allow a reduction in dose of prodrug, and thus of systemic sidefects. Nucleic acids encoding the agent may be expressed selectively protein vectors the HSV-1 tegument protein vectors this is used in the construction of a fusion protein comprising vP22 and a human P450 reductase derivative alp450R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardiovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; graft; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis; tachycardia; HIV-1.
                                                                                                                                                                                                                                                                                                                                                                          invention provides a new prodrug activating agent that comprises: (i)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 QLWDMSRPRTDEDLNELLGITIRVTVCEGRNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                   New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV, 60
                                                                           Griffiths L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                           Patterson AV, Kingsman SM, Kan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 738; DB 20;
Pred. No. 7.4e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW95099 standard; Protein; 301 AA.
                                                                                                                                                                                                                                                                                                                    Example 7; Fig 3D; 149pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 ASRPTERPRAPARSASRPRRPVE 143
                      (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV-1 VP22 polypeptide.
                                                                                                                                                       WPI; 1999-540852/45.
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                                                                                                                                                                                N-PSDB; AAZ07807
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Matches 143;

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Query Match

Sequence

Human immunodeficiency virus type 1.

AAW95099;

RESULT 4 AAW95099

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Length 301; Indels

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Howley P, Benson J,
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                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ88468
                                                                                                                             WO200001720-A2
                                                                                                                                                                                               02-JUL-1999;
                                                                                                                                                                                                                              02-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-NOV-2001
                                                                                                                                                              13-JAN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                279
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ID AAB6
XX
AC AAB6
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DT 05-N
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                                                                                                                                                                                                                                                                                                                                                                                                                    The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a call linked to the interaction domain of the ubiquitin ligase. Such methods are useful for decreasing or conceasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a call is subjected to SCF abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of concoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the mature animal. The hybrid ubiquitin ligase may also include an consideration sequence such as this HSV-1 V22 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                          Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ublquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; . Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 738; DB 21; Length 301; 100.0%; Pred. No. 7.4e-76; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 76; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY79877 standard; Peptide; 301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US23705
                                                                                                                                                            98US-0103787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                           (HARD ) HARVARD COLLEGE
                           Herpes simplex virus-1.
                                                                                                                                                                                                                                                           WPI; 2000-317970/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSV-1 VP22 peptide.
                                                                                                                                                                                                                            Howley P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 AA;
                                                                                                                                                                                                                                                                            N-PSDB; AAZ93717
                                                            WO200022110-A2
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                                                                                                                                                           09-0CT-1998;
                                                                                           20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 143;
            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence
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                                                                                                                                                                                                                          Zhou P,
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The present invention describes the use of a small organic compound (A) which competitively inhibits interaction of a papillomavirus (PV) E2 protein with a PV E1 protein for treating a cell infected with PV or a mammal with a PV E1 protein for treating a cell infected with PV or a captostatic, antiproliferative and dermatological activities. Methods from the present invention can be used to treat PV-induced conditions including growth of PV preneoplastic and neoplastic lesions, cutaneous including growth of PV preneoplastic and neoplastic lesions, cutaneous lesions chosen from warts and other benign cutaneous lesions, plantar warts (verruca plana), Butcher's common warts, flat warts, genital warts (condyloma acuminatum) and epidermodysplasta verruciformis), laryngeal, oral, pharyngeal, cervical, cepidermodysplasta verruciformis, laryngeal, oral, pharyngeal, orsophageal and other upper airway papilloma or vaginal, cervical, vulvar, penile and anorectal carcinoma. The E2 inhibitors may also be used to treat epithelial and internal fibropapillomas in animals.

The present sequence represents a peptide sequence used in the exemplification of the present invention.
        E2; peptidomimetic; ive; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Use of papillomavirus E2 protein peptidomimetics for treating papillomavirus-infected cells and papillomavirus-induced conditions in mammals by inhibiting E1-E2 interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
Papillomavirus; PV; infection; cell proliferation; E2; peptidomis E1; antiviral; virucide; cytostatic; antiproliferative; dermatcol: preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart; epidermodysplasia verruciformis; anorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 301;
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100.0%; Pred. No. 7.4e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 42; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB60910 standard; Protein; 301 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ASRPTERPRAPARSASRPRRPVE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0091661.
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                                                                                                                                                                                                                       Herpes simplex virus type
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Matches 143; Conservative
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RESULT 6 AAY7987

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This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for immunising an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and its encoding DNA (I) for immunizing an individual against diseases, in particular against infection-induced auto-immune and tumor disease. This sequence represents the VP22 protein fragment used in the construction of the fusion construct VP22-E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2; antidiabetic; apoptosis; inhibitor; cellular uptake; anti-apoptosis; ischaemic disease; myocardial infarct; ANDS; neurodegenerative diseases; infective multiple failure; fulminant hepatitis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying an immunization agent comprising cell import and/c export signal sequences and an antigen for immunizing against infection-induced auto-immune and tumor disease
      Fusion protein; VP22; E7; cell import signal; cell export signation; immunization; infection-induced auto-immune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                            Sentgraf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 738; DB 22;
100.0%; Pred. No. 7.4e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            ľ,
                                                                                                                                                                                                                                                                                                                                                            Gissmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Herpes simplex viral protein: SEQ ID 26
                                                                                                                                                                                                                                                                                                                (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG64275 standard; protein; 301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 ASRPTERPRAPARSASRPRRPVE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                         Osen W,
                                                                                                                                                                                                                         15-JAN-2001; 2001WO-DE00134.
                                                                                                                                                                                                                                                                     13-JAN-2000; 2000DE-1001230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442135/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 AA;
                                                                                                                                       WO200151516-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200148014-A1
                                                tumor disease.
                                                                                             Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-SEP-2001
                                                                                                                                                                                19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                         Mueller M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG64275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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      δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method of identifying the co-activator domain of specific synthetic activators, involving contacting the target domain of a selected transcription factor with a peptide display library, and identifying those sequences which bind to the target domain. In particular, those which bind to the KIX domain of p300/CBP are useful. The peptides can be used in the treatment of diseases related to aberrant KIX-dependent gene transcription, including erythrocythaemia, penyphian haemoglobinopathies, to regulate cell differentiation, to treat neurological diseases, immunological diseases, diabetes, ulcers, skin diseases and cancer, and to aid wound healing. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρλ
                                           Co-activator domain; P300/CBP KIX domain; erythrocythaemia; skin dise polycythaemia; haemoglobinopathy; cell differentiation; ulcer; cancer neurological condition; neurodegenerative disease; immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying co-activator domain specific transcriptional activators b contacting a target domain of a selected transcription factor with a peptide display library, where the identified binding peptides are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 738; DB 22;
100.0%; Pred. No. 7.4e-76;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Montminy MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 78; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB86329 standard; Protein; 301 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for reducing hyperglycemia
                                                                                                                                                                                                                                                                                                                                                                                                JOSLIN DIABETES CENT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-AUG-2000; 2000WO-US24010.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Cantley LC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-273380/28.
HSV-1 VP22 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAF58996
                                                                                                                                                                                                WO200118036-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Frangioni JV,
                                                                                                                                                                                                                                                                                                                                                                            (BETH-) BETH
                                                                                                                                                                                                                                           15-MAR-2001
                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                             diabetes
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RESULT 8 AAB86329

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Virucide; cytostatic; vaccine; intercellular transport; antigenic; immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3-VP22/E7; chronic viral infection; veterinary herpesvirus infection; pseudorables; equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a cdc4 phospho design (CPD) motif, (C), that targets molecules for ubiquitin dependent proteolysis. (C) have eytostatic, noctropic and antiproliferative activity. Also described is a method for the treatment of a disease or condition where affective feels have a defective protein, comprising administering (C) to promote degradation of the target protein in cells by ubiquitin dependent proteolysis. (C) can also be used for modulating the proliferation, growth and/or differentiation of cells. (C) can be used to modulate ubiquitin dependent proteolysis or cell proliferation, growth and or differentiation of cells. (C) is useful in the treatment of cancers and neurodegenerative disorders as well as spinal degeneration. The present sequence represents the HSV-1 VP22 protein which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..301
/note= "VP22 transport polypeptide from herpes simplex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                          New Cdc4 Phospho Design motif that targets molecules for ubiquitin dependent proteolysis, is useful for the modulation of cell proliferation i.e. cancer treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fowl; animal retroviral disease; rabies; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 738; DB 23; Best Local Similarity 100.0%; Pred. No. 7.4e-76; Matches 143; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric – herpes simplex virus type 1.
Chimeric – human papilloma virus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PcDNA3-VP22/E7 fusion protein sequence.
                                                                                                                                 Tyers M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ą.
                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 30; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU77235 standard; Protein; 418
                                                                                    (MOUN ) MOUNT SINAI HOSPITAL.
                      04-MAY-2000; 2000US-202166P.
24-JAN-2001; 2001US-263774P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                          2002-164074/21.
                                                                                                                                 Pawson T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AA;
                                                                                                                                                                                                   N-PSDB; ABA93386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric -
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU77235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                               Nash P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
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AAU77235
    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to BH4-fused polypeptides. The BH4-fused polypeptide have a sequence capable of affecting cellular uptake and also a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The BH4-fused polypeptides are useful as effective apoptosis inhibitors, and are useful in preventives or remediaes for ischaemic diseases e.g. myocardial infarct, AIDS, neurodegenerative diseases, infective multiple failure, fulminant hepatitis and diabetes. The present peptide was used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif; CDP motif; cytostatic; nootropic; antiproliferative; cell proliferation; growth; differentiation; cancer; neurodegenerative disorder;
                                                                                                                                                                                                                                                            BH4-fused polypeptides with peptide sequences capable of exerting effect on enabling uptake into cells, applicable as effective apoptosis inhibitors, useful in preventives or remedies for ischemic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 301;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 738; DB 22; 100.0%; Pred. No. 7.4e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  · ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by CAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Claim 5; Page 74-6; 84pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                         26-DEC-2000; 2000WO-JP09274
                                                                                    99JP-0371449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-MAY-2001; 2001WO-CA00632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-APR-2002 (first entry)
                                                                                                                               (SHIO ) SHIONOGI & CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                          Tsujimoto Y;
                                                                                                                                                                                                                                                                                                                            e.g. myocardial infarct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spinal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus
                                                                                                                                                                                                                   WPI; 2001-418246/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSV-1 VP22 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200183518-A2
                                                                                    27-DEC-1999;
05-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 143;
                                                                                                                                                                          Shimizu S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB05524;
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Seguence Query Match Best Local

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RESULT 10 ABB05524

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Gaps

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Using site-specific DNA recombinase domain/protein transduction domain fusion proteins for inducing target gene alterations in organisms or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is delta VP22Cre-StrepTag fusion protein. The VP22 sequence is from Human spumaretrovirus (HSV).
                                                                            DNA recombinase domain; protein transduction domain; PTD; gene alteration; delta VP22Cre-StrepTag fusion protein; Human immunodeficiency virus; HIV; Human spumaretrovirus; HSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA recombinase domain; protein transduction domain; PTD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 738; DB 22;
100.0%; Pred. No. 1.6e-75;
iive 0; Mismatches 0;
                                         Delta VP22Cre-StrepTag fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 46-47; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE05266 standard; Protein; 667 AA.
                                                                                                                                                         Chimeric - Human spumaretrovirus.
Chimeric - Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ASRPTERPRAPARSASRPRRPVE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASRPTERPRAPARSASRPRRPVE 157
                                                                                                                                                                                                                                                                                                                                     07-JAN-2000; 2000EP-0100351.
10-NOV-2000; 2000EP-0124595.
                                                                                                                                                                                                                                                                                                05-JAN-2001; 2001WO-EP00060
                                                                                                                                                                                                                                                                                                                                                                                                  (ARTE-) ARTEMIS PHARM GMBH.
12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 143; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VP22-Cre fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Using site-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-441873/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          539 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAD09263
                                                                                                                                                                                                                   WO200149832-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell cultures
                                                                                                                                                                                                                                                           12-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Schwenk F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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AAE05266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infections, including equine or bovine herpesvirus, Marek's disease virus in chickens and other fowls, animal retroviral diseases, pseudorables and rables. The present amino acid sequence represents the pcDNA3-VP22/F7 fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a new nucleic acid molecule that encodes a fusion polypeptide. The fusion protein comprises a first polypeptide comprising at least one intercellular transport polypeptide and a second polypeptide comprising at least one antigenic polypeptide or peptide. The invention also describes an optional linker peptide intring the first and second polypeptide. The nucleic acid is useful as a vaccine for enhancing immune responses, primarily cytotoxic T lymphocyte responses to specific antigens such as tumour or viral antigens. The compositions comprising the nucleic acids are especially
virus type 1, specifically claimed in claim 10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding fusion polypeptide comprising intercellular transport polypeptide linked to antigenic polypeptide, useful as therapeutic vaccine for cancer and major chronic viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                useful as a therapeutic vaccine for cancer and for major chronic viral infections, as well as in the treatment of veterinary herpesvirus
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                                                                                               human papilloma virus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 738; DB 23;
Pred. No. 1.1e-75;
                                                                              the
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100.0%; Pred. No. 1...
0; Mismatches
                                                                            "Represents 96 of
                                       "Linker sequence"
                                                                                                                                    /note= "Vector sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-2000; 2000US-222185P.
15-FEB-2001; 2001US-268575P.
04-APR-2001; 2001US-281004P.
                                                                                                                                                                                                                                                       01-AUG-2001; 2001WO-US23966
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                  . 307
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                                                                                                                  404..418
                                       /note=
308..40
                                                                              /note=
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N-PSDB; ABK11810.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Hung C;
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Gaps

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Length 539; Indels

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WPI; 2001-441873/47.
                                                                                                                                                                             Using site-specific fusion proteins for
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Matches 143; Conserv
                                                                                                                                                                                                                                                                                                                                             683 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene alteration;
                                                                                                                                                          N-PSDB; AAD09268
            WO200149832-A2.
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                                                                                                                                                                                                   cell cultures
                                                                         07-JAN-2000;
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                                12-JUL-2001
                                                                                                                             Schwenk F;
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gene alteration; VP22-Cre fusion protein; Human immunodeficiency virus;
                                                                                                                                                                                                                               DNA recombinase domain/protein transduction domain inducing target gene alterations in organisms or
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0;; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA recombinase domain; protein transduction domain; PTD; VP22CreStrepTag fusion protein; Human immunodeficiency virus; HIV; gene alteration; Human spumaretrovirus; HSV.
                                                                                                                                                                                                                                                                                         The present invention relates to use of fusion proteins comprising
                                                                                                                                                                                                                                                                                                 a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP22-Cre fusion protein. The
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                           VP22 sequence is from Human spumaretrovirus (HSV)
                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 738; DB 22; 100.0%; Pred. No. 2.1e-75;
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                                                                                                                                                                                                                                                                     Claim 12; Page 35-37; 85pp; English.
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                               Chimeric - Human spumaretrovirus
Chimeric - Unidentified.
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Chimeric - Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE05273 standard; Protein; 683
           HIV; Human spumaretrovirus; HSV
                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VP22CreStrepTag fusion protein.
                                                                                                                         07-JAN-2000; 2000EP-0100351
10-NOV-2000; 2000EP-0124595
                                                                                                      05-JAN-2001; 2001WO-EP00060
                                                                                                                                                         (ARTE-) ARTEMIS PHARM GMBH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                               WPI; 2001-441873/47.
                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                             667 AA;
                                                                                                                                                                                                         N-PSDB; AAD09259
                                                             WO200149832-A2.
                                                                                                                                                                                                                                                  cell cultures
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                                                                                 12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 143;
                                                                                                                                                                             Schwenk F;
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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VP22-Flpe fusion protein; Human immunodeficiency virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP22CreStrePTag fusion protein. The VP22 sequence is from Human spummaretrovirus (HSV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 738; DB 22; Length 683; 100.0%; Pred. No. 2.2e-75; tive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA recombinase domain; protein transduction domain; PTD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 58-60; 85pp; English.
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05-JAN-2001; 2001WO-EP00060
                                                                   07-JAN-2000; 2000EP-0100351.
10-NOV-2000; 2000EP-0124595.
                                                                                                                                                                                    (ARTE-) ARTEMIS PHARM GMBH.
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Conservative
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05-JAN-2001; 2001WO-EP00060

2000EP-0100351 2000EP-0124595

07-JAN-2000; 10-NOV-2000;

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                                                                                                                                                                                        Using site-specific DNA recombinase domain/protein transduction domain fusion proteins for inducing target gene alterations in organisms or cell cultures.
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                                                                                                                                                                                                                                                                                                  fusion proteins comprising
                                                                                                                                                                                                                                                                                             The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP22-Fipe fusion proteins of the NP22 sequence is from Human spummaretrovirus (HSV).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 747;
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                                                                                                                                                                                                                                                              Claim 12; Page 40-43; 85pp; English.
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                                                                                (ARTE-) ARTEMIS PHARM GMBH.
                                                                                                                                              WPI; 2001-441873/47.
N-PSDB; AAD09260.
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                                                                                                               Schwenk F;
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Sequence Sequence Sequence

Total number

Database

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searched:

Sequence:

OM protein

Run on:

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STAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08303861
Patent No. 6086902
GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
TITLE OF ENVENTION: VACCINES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 738; DB 3;
Pred. No. 4e-79;
Mismatches 0;
                                   US-09-230 421-4

US-09-211-704A-8

US-09-211-704A-8

US-09-521-220-3

US-09-391-104-29

US-09-313-409-6

US-09-568-102-6

US-09-568-102-6

US-09-568-480-6

US-09-568-480-6
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                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TROBE PC CO
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755 Page Mill Road
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NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
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TELEX: 706141
:NFORMATION FOR SEQ ID NO: 21:
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TELEFAX: (415) 494-0792
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Best Local Similarity
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US-08-303-861-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-303-861-21
LENGTH:
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                                                                                                                                   21, 2003, 17:33:24 ; Search time 12.2387 Seconds. (without alignments) 343.784 Million cell updates/sec
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Compugen Ltd.
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             GenCore version Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Perfect score:
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Maximum DB seq
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Best Local Similarity
Matches 143; Conserv
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US-09-347-504-12
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Best Local S
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                              219 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 278
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                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: O'Hare et al.
TITLE OF INVENTON: TRANSPORT PROTEINS AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  ADDRESSEE: Klarquist Sparkman Campbell Leigh
ADDRESSEE: Whinston, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 738; DB 4;
; Pred. No. 4e-79;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Earp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5759-49294/DJE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,073A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States of America ZIP: 97204-2988 COMPUTER READABLE FORM: MEDIUM TYPE: Disk, 3-1/2 inch COMPUTER: IBM FC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
                                                                                                                                                                                                                                                                                                               ADDRESSEE: Whinston, LLP
STREET: One World Trade Center
STREET: 121 S W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
                                                                                                                                                                                    Sequence 1, Application US/09011073A Patent No. 6184038
                                                                         121 ASRPTERPRAPARSASRPRRPVE 143
                                                                                             121 ASRPTERPRAPARSASRPRRPVE 143
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100.0%;
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TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 143; Conservative
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TOPOLOGY: linear
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US-09-011-073A-1
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61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSA 120
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Sequence 12, Application US/09347504

Patent No. 6399075

GENERAL INFORMATION:
APPLICANT: Howley, Peter M.
APPLICANT: Benson, John
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REPERENCE: HWV-041.01

CURRENT APPLICATION NUMBER: US/09/347,504

CURRENT FILING DATE: 1999-07-02

NUMBER OF SEQ ID NOS: 79

SOSTUMBER DEACHIN Ver. 2.1

SED ID NO 12

LEMPROLECE

SEQ ID NO 12
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99.3%; Pred. No. 3.5e-78;
ive 0; Mismatches 1; Indels
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Patent NO. 6200577
GENERAL INFORMATION: GENERAL INFORMATION: APPLICANY: Medical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REPERENCE: P18189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 73%; DB 4;
100.0%; Pred. No. 4e-79;
tive 0; Mismatches (
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Matches 142, Conservative
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TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
TITLE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
FILE REFERENCE: WSHU 2001
CURRENT APPLICATION NUMBER: US/09/336,093A
CURRENT FILING DATE: 1999-06-18
NUMBER OF SEO ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SEO ID NO 5
LENGTH: 246
TYPE: PRT
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US-09-230-421-3
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                                                                    GENERAL INFORMATION:
APPLICANT: 'Medical Research Council
TILE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P18189C
CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SOD ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.0
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100.0%; Pred. No. 1.3e-59;
tive 0; Mismatches 0;
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Pred. No. 4.8e-41;
3; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 DAATATRGRSAASRPTERPRAPARSASRPRRVE 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Herpes simplex virus VP22 protein US-09-336-093-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/09336093A Patent No. 6348185
                                        Sequence 3, Application US/09230421
Patent No. 6200577
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                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.1%
Best Local Similarity 100.0
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 64.3 Matches 99; Conservative
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                                                                                                                                                                                                                                                                SEQ ID NO 3
LENGIH: 144
RESULT 5
US-09-230-421-3
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                                                                                                                                                                                                                                                                                                          TYPE: PRT
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127 AVGPPRPRAPPGANAVASGRPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVALVAAEYAR 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 STAPTRSKTP----AQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHAR 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 258;
                                                                                                                 TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE TITLE OF INVENTION: VACCINES NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECOMBINANT BOVINE HERPESVIRUS TYPE VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/2019 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 210; DB 3;
Pred. No. 7.2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29310-20020.20
                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                : MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/08303861
Patent No. 6086902
GENBEL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
Sequence 18, Application US/08303861
Patent No. 6086902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFRENCE/DOCKET NUMBER: 2931(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.5%;
34.1%;
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APPLICANT: BABIUK, LORNE A.
TITLE OF INVENTION: RECOMBI
TITLE OF INVENTION: VACCINE
                                                                                                     BABIUK, LORNE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 258 amino acids
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                                                             ZAMB, TIMOTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 706141
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein US-08-303-861-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTIC:
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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California
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Best Local Similarity
Matches 45; Conserv
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                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                ADDRESSEE:
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US-08-303-861-19
                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                              APPLICANT:
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                                                           APPLICANT
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STATE:
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57 MAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQDVDAATATR 116
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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California
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US-09-347-504-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63; Indels
                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Harms, Jerome S.

PEPLICANT: Splitter, Gary A.

TITLE OF INVENTION: Biotherapeutic Delivery System
FILE REFERENCE: 960296,95564

CURRENT APPLICATION NUMBER: US/09/213,343

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatenLIN Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28.5%; Score 210; DB 3; 34.1%; Pred. No. 7.2e-17; tive 20; Mismatches 63
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 29310-20020.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPROSE: (415) 494-0792
                                                                                                                                                                                         APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09213343 Patent No. 6316252 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    TELEFAX: (412,
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                        IBM PC compatible
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bovine herpesvirus 1 US-09-213-343-2
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45; Conservative
                CITY: Palo Alto
STATE: California
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Matches 45; Conserva
                                                   RY: USA
94304-1018
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US-08-303-861-19
                                                   COUNTRY:
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199 AAWNSNPPRNNAELDRLLTGAVIRITVHEGLNLIQAANEADLGEGASVSKRGHNRKTGDL 258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 QLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANE-------99
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                                                                                                                                                                                                                                                                                                           APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: LIANG, XIAOPING
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE I
TITLE OF INVENTION: VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 ---LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 137
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; Pred. No. 3.5e-16;
18; Mismatches 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS.
                                                                                                                                                                                                           US-08-303-861-20
; Sequence 20, Application US/08303861
; Patent No. 6086902
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page M111 Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 14, Application US/09347504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K,
REGISTRATION NUMBER: 35,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 2
TELECOMMUNICATION INFORMATION
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302 amino acids
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Best Local Similarity 34.8%
Matches 56; Conservative
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us-09-522-278b-12.rag

GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd..

OM protein · protein search, using sw model

Run on:

May 21, 2003, 17:13:44 ; Search time 73.2162 Seconds (without alignments) 547.808 Million cell updates/sec

US-09-522-278B-12 1561 1 MTSRRSVKSGPREVPRDEYE......PTERPRAPARSASRPRRFVE 301 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

908470 segs, 133250620 residues Searched:

908470

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Jcgdata/geneseg/genesegp-embl/AA1988 /SIDS2/gcgdata/geneseg/genesegp-emb1/AA198 /gcgdata/geneseq/geneseqp-embl /gcgdata/geneseg/genesegp-emb. /SIDS2/gcgdata/geneseq/geneseqp//SIDS2/gcgdata/geneseq/geneseq/ Post-processing: Minjmum Match 0% Maximum Match 100% Listing first 45 summaries SIDS2 IDS: SIDS Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT 'qcqdata/qeneseq/qeneseqp-emb]/AA1999 IDS2 IDS2 DS: IDS

gcgdata/geneseq/geneseqp-embl/AA199

gcgdata/geneseg/genesegp-emb]

IDS

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Herpes simplex vir	HSV-1 tequment pro	VP22 protein fragm	Herpes simplex vir	VP22-Cre fusion pr	VP22-F1pe fusion p	PCDNA3-VP22/E7 fus	VP22CreStrepTag fu	HIV-1 VP22 polypep	HSV-1 VP22 peptide
		ID	1 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AA142232	AAY27404	AAB86329	AAG64275	AAE05266	AAE05267	AAU77235	AAE05273	AAW95099	AAY79877
		DB	: 6	?	20	22	22.	22	22	23	22	20	21
		Match Length DB		30T	301	301.	301	299	747	418	683	301	301
dР	Query	Match		7.00	100.0	100.0	100.0	100.0	100.0	7.66	7.66	99.66	99.66
		Score	1 1 2 2 2 2	TOCT	1561	1561	1561	1561	1561	1557	1557	1554	1554
	Result	NO.		-	7	e	4	S	9	7	œ	6	10

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AAB60910 AAB05524 AAW83261 AAW83261 AAW83261 AAW86330 AAB60521 AAW72068 AAW72068 AAW72068 AAW72069 AAW72069 AAW72069 AAW72069 AAW72069 AAW72069 AAW72069	AMB05525 AMW2663 AMW2663 AAM51320 AAM48195 AAM68520 AAM68528 AAM178347 AAU78347
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3301 3001 3001 3001 3006 3006 3006 3006	37 1399 1399 388 388 451 344 354
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1554 1554 1553 1553 1553 1520 1003 573 673 673 772 271 271 573 773 774 179 179	179 172.5 172.5 172.5 168.5 168.5 168.5 164
	2 6 6 7 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9

Key Misc-difference 251267 Mote= "Corresponding DNA sequence appears to be absent" M09945127-A2. 10-SEP-1999. 05-MAR-1999; 99MO-GB00674. 06-MAR-1998; 98GB-0004841. 19-AuG-1998; 98GB-0018103. 29-JAN-1999; 99GB-0018103.
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                                                                                                                                                         The sequence represents a merges simples vitus cype I (MSVI)

VP22 tegument protein, which is involved in transcellular

localisation. VP22 can be fused to cytochrome P450 reductase (P450R)

derivatives such as anchorless P450R (AAV42281) or FN fragment

(AAV4228B). This enables the fusion protein to be delivered to

neighbouring cells where it is then transported to the nucleus. Many

drugs's sites of action are in the nucleus, rather than the cytoplasm,

where P450R normally functions. P450R or its derivatives can be used to

activate prodrugs to their active form via reduction. Administration of a

crivate prodrugs to their active form wis reduction. Administration of a

crivate prodrugs to their active form wis reduction. Administration of a

activate prodrugs active drug may be metabolised before it

reaches its site of action or where the active drug is cytotoxic, e.g.

anticancer drugs. Targetted delivery of such prodrug activators allows

anticancer drugs. Targetted delivery of such prodrug activators allows

reduction in dose of the prodrug, and thus of systemal cide-effects.

P450R derivative fusion proteins, or vectors that express them, are

specifically used to treat tumours, inflammation, atherosclerosis and

muscular dystrophy, but may also be used to treat many other conditions,

e.g., cerebral malaria, rheumatoid arthritis, or conditions associated

with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics,

antitional astic and diagnost is ancesthetics, anti-inflammatories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPAGSGGÄGRTPTTAPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                           or tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 APPNPDAPWTPRVAGENKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV
                                                                                                                                                   sequence represents a Herpes simplex virus type 1 (HSV-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1561; DB 20; Length 301; llarity 100.0%; Pred. No. 6.4e-122; Conservative 0; Mismatches 0; Indels 0;
                                                                       New prodrug activating agent targeted to selected cells particularly hypoxic cells, for treating e.g. tumors -
                                                                                                                                                                                                                                                                                                                                                                                                                                   antineoplastic agents and diagnostic agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY27404 standard; Protein; 301 AA.
                                                                                                                     Example 7; Fig 3; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSV-1 tegument protein VP22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                            WPI; 1999-551046/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AA;
                                           N-PSDB; AA219784
Mitrophanous K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Simi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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AAY27404
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Trigoritis provises a may produce acceptive antibody) and a product activation domain (DB): (ii) at least one nucleic acid encoding a cytochrome p450 and under control of at least one nucleic acid encoding a cytochrome p450 and under control of a least one constitutive or control sequence or (iii) a modified hematopoletic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and under control of elements as in (ii). The prodrug activating agent or under control of elements as in (ii). The prodrug activating agent or cortors that express them, are specifically used to treat tumors, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g. cerebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, hypoglycemia or sachetics, anti-inflammatories, anti-neoplastic agents and diagnostic agents. LD optimize activity of PAD, e.g. by delivering it to neighboring cells (hystander effect), and allow a reduction in dose of prodrug, and thus of systemic aiderefects. Nucleic acids encoding the agent may be expressed selectively comparising vP22. This is used in the construction of a fusion protien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                Location/Qualiflers
251..267
/note= "the corresponding DNA sequence for this region
/note= "the corresponding" there are only 4 nucleotide
basepairs indicated as encoding for this entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides a new prodrug activating agent that comprises: (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 APRTORVATKAPAAPAAETTRGRKSAOPESAALPDAPASTAPTRSKTPAOGLARKLHFST 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation
                                      inflammation; atherosclerosis; muscular dystrophy; cerebral malaria; rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; HSV; VP22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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modified hematopoletic stem cell; MHSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patterson AV, Kingsman SM, Kan O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 1561; DB 20;
100.0%; Pred. No. 6.4e-122;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7; Fig 3D; 149pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                   Herpes simplex virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB00672.
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   activating domain;
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Best Local Similarity 100.
Matches 301; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-540852/45.
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                                                                                                              tegument protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mitrophanous K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stratford IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9945126-A2
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29-JAN-1999;
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                                                                                                                                                                                                                                                                                                  Region
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AAG64275 standard; protein; 301 AA.

AAG64275

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IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV

APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT

180

DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

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This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for immunizing an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and tas encoding DNA (I) for immunizing an individual against diseases, in particular against infection-induce auto-immune and tumor disease. This sequence represents the VP22 protein fragment used in the construction of
241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
                                                                                                                                                                                                                                                                                                                                antigen; immunization; infection-induced auto-immune disease; tumor disease.
                                       APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying an immunization agent comprising cell import and/cexport signal sequences and an antigen for immunizing against infection-induced auto-immune and tumor disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zentgraf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1561; DB 22;
llarity 100.0%; Pred. No. 6.4e-122;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gissmann L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 4; 23pp; German.
                                                                                                                                                                                                                                 AAB86329 standard; Protein; 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JAN-2000; 2000DE-1001230.
                                                                                                                                                                                                                                                                                                             VP22 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Michel N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-442135/47.
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                                                                                                                                                                                                                                                                                                                                                                                          Unidentifled
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                                                                                                                                          E 301
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                                                                                                                                                                 E 301
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Best Local
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BH4 domain; cardiant; anti-HIV; neuroprotective; hepatotropic; Bcl-2; antidiabetic; apoptosis inhibitor; cellular uptake; anti-apoptosis; ischaemic disease; myocardial infarct; AIDS; neurodegenerative diseases; infective multiple failure; fulminant hepatitis; diabetes.

Herpes simplex virus type 1.

WO200148014-A1.

05-JUL-2001.

26-DEC-2000; 2000WO-JP09274

Herpes simplex viral protein: SEQ ID 26.

(first entry)

21-SEP-2001

AAG64275;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to BH4-fused polypeptides. The BH4-fused polypeptide have a sequence capable of affecting cellular uptake and also a BH4 domain sequence from an anti-apoptosis Bcl-2 family protein. The BH4-fused polypeptides are useful as effective apoptosis inhibitors, and are useful in preventives or remedies for ischaemic diseases e.g. myocardial infarct, AIDS, neurodegenerative diseases, infective multiple failure, fulminant hepatitis and diabetes. The present peptide was used
                                                                                                                                                                                                                                                                                                                                                                BH4-fused polypeptides with peptide sequences capable of exerting effect on enabling uptake into cells, applicable as effective apoptosis inhibitors, useful in preventives or remedies for ischemic diseases e.g. myocardial infarct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1561; DB 22;
100.0%; Pred. No. 6.4e-122;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 74-6; 84pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                  (SHIO ) SHIONOGI & CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in the present invention.
                                                                                                                                                                                                                                                                                                             Tsujimoto Y;
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-418246/44.
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Best Local Simil
Matches 301; C
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                                                                                                                                                                                                                                                                                                            Shimizu
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MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

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DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120

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1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

Matches 301;

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Sequence
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                                                                                                                                                                                                                                                                                                                                          DNA recombinase domain; protein transduction domain; PTD;
gene alteration; VP22-Cre fusion protein; Human immunodeficiency virus;
HIV; Human spumaretrovirus; HSV.
                                                                                                           240
                                                                                                                                240
                                                                                                                                                  180
                             120
                                                                   121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to use of fusion proteins comprising a site-specific DNA recombinase domain e.g. cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism call culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP22-cre fusion proteins of the VP22 sequence is from Human spummaretrovirus (HSV).
                                                                                                                     DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPAGSGGAGRIPTTAPR
                                      61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR
                                                                             121 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST
                                                                                                            APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Using site-specific DNA recombinase domain/protein transduction de
fusion proteins for inducing target gene alterations in organisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 35-37; 85pp; English.
                                                                                                                                                                                                                                                             AAE05266 standard; Protein; 667 AA
                                                                                                                                                                                                                                                                                                                                                                                Chimeric - Human spumaretrovirus.
Chimeric - Unidentified.
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10-NOV-2000; 2000EP-0124595.
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                                                                                                                                                                                                                                                                                                                       VP22-Cre fusion protein.
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N-PSDB; AAD09259.
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DNA recombinase domain; protein transduction domain; PTD; gene alteration; VP22-Flpe fusion protein; Human immunodeficiency virus; HIV; Human spumaretrovirus; HSV.
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                                                                                                          181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
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      Length 667;
                                             Indels
    Score 1561; DB 22;
Pred. No. 1.7e-121;
Mismatches 0;
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Chimeric - Unidentified.
100.0%; Sc
100.0%; Pr
tive 0;
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10-NOV-2000; 2000EP-0124595
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                                               Conservative
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    Query Match
Best Local Similarity
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                                               Matches 301;
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01-AUG-2001; 2001WO-US23966.
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15-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune response; cytotoxic T lymphocyte; tumour; cancer; pcDNA3 vP22/E7; chronic viral infection; veterinary herpesvirus infection; pseudorables; equine herpesvirus; bovine herpesvirus; Marek's disease virus; chicken;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "VP22 transport polypeptide from herpes simplex virus type 1, specifically claimed in claim 10"
                                                                                                                                                                                              180
                                                                                                                                                          DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
                                                                                                                                                                                                                                                                       IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
                                                                                                     Gaps
                                                                                                                                       9
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                                                                                                                                                                                             target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP22-Fipe fusion protein. The VP22 sequence is from Human spummaretrovirus (HSV).
                                                                                                                                1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
                                                                                                                                                                                                                                  APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
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for preparing an agent for inducing
                                                                                  Length 747;
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                                                                                 Score 1561; DB 22; Length
Pred. No. 2e-121;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fowl; animal retroviral disease; rabies; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human papilloma virus type 16
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                                                                                100.0%;
derived TAT peptide,
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                                                                                                     Matches 301; Conservative
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                                                                                 Query Match
Best Local Similarity
                                                               747 AA;
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                                                               Sequence
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The present invention relates to a new nucleic acid molecule that
encodes a fusion polypeptide. The fusion protein comprises a first
encodes a fusion polypeptide. The fusion protein comprises a first
comprising at least one intercellular transport polypeptide
and a second polypeptide comprising at least one artigenic polypeptide
corporated. The invention also describes an optional linker peptide
corporated second polypeptide. The nucleic polypeptide
corporated second polypeptide as a vaccine for enhancing immune responses, primarily cytoroxic T
corporated second polypeptide antigens such as tumour or viral
corporated second polypeptide antigens such as tumour or viral
corporated second polypeptide antigens such as tumour or viral
corporated second polypeptide antigens such as a therapeutic vaccine for cancer and for major chronic viral
corporated second polypeptide animal retroviral diseases, pseudorabies
conditions, including equine or bovine herpesvirus, marek's disease virus
conditions. The present amino acid sequence represents the pcDNA3-VP22/E7
corporated second polypeptide.
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                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding fusion polypeptide comprising intercellular transport polypeptide linked to antigenic polypeptide, useful as therapeutic vaccine for cancer and major chronic viral infections -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 7; 102pp; English.
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15-FEB-2001; 2001US-268575P.
04-APR-2001; 2001US-281004P.
                                                                                                          SNINGO NINIV JOHNS HOPKINS
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AAW95099 standard; Protein; 301
                                                                              25-MAY-1999 (first entry)
                                                        AAW95099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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                                           DNA recombinase domain; protein transduction domain; PTD; VP22CreStrepTag fusion protein; Human immunodeficiency virus; HIV; gene alteration; Human spumaretrovirus; HSV.
                                                                                                                                                                                                                                                                                                                                                                           a site-specific DNA recombinase domain e.g. Cre and a protein transduction domain (PTD) e.g. the Human immunodeficiency virus (HIV) derived TAT peptide, for preparing an agent for inducing target gene alterations in a living organism or cell culture. The present invention also provides a method for inducing gene alterations in living organisms using the fusion proteins of the invention. The present sequence is VP2CzrcstrepTag fusion protein. The VP22 sequence is from Human spumaretrovirus (HSV).
                                                                                                                                                                                                                                                                                                                                                                    present invention relates to use of fusion proteins comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.7%; Score 1557; DB 22; Length 683; Best Local Similarity 99.7%; Pred. No. 3.8e-121; Matches 300; Conservative 1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 58-60; 85pp; English.
                                                                                       Chimeric – Human spumaretrovirus.
Chimeric – Unidentified.
                     VP22CreStrepTag fusion protein.
                                                                                                                                                                                      2000EP-0100351.
2000EP-0124595.
                                                                                                                                                                   05-JAN-2001; 2001WO-EP00060
                                                                                                                                                                                                                       (ARTE-) ARTEMIS PHARM GMBH.
(first entry)
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N-PSDB; AAD09268.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             683 AA;
                                                                                                                        WO200149832-A2.
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10-NOV-2000;
12-SEP-2001
                                                                                                                                             12-JUL-2001
                                                                                                                                                                                                                                             Schwenk F;
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CODES), particularly CDK/cyclin complexes. It provides a recombinant transfection system (A) that comprises: (1) first gene construct comprising a sequence encoding an inhibitory polypeptide conceining at least one CDK-binding motif for binding and inhibiting activity of a CDK, linked to a transcription regulator functional in eukaryotic cells; (11) second agene construct comprising a sequence encoding a polypeptide that promotes endothelialisation, and (iii) a gene delivery composition for delivering the GCs to a cell for transfection. Also provided are nucleic acids encoding a fusion protein (FP) containing: (1) a therapeutic polypeptide sequence (TP) from an intracellular process when FP enters the cell, and (ii) a therapeutic polypeptide sequence (TP) from an intracellular process when FP enters the cell, and (ii) a transcellular polypeptide sequence (TCP) that promotes transcytosis of FP. The FP consists of at least one CDK-binding motif and a TCP. See AXX26220 for detailed uses of the recombinant transfection system. The CKI FDIypeptides are engineered to include any of the peptides shown in
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                                                                           Cyclin-dependent kinase; CDK; CDK/cyclin complex; inhibitory; restenosis; CDK-binding motif; endothelialisation; fusion protein; therapeutic; acne; intracellular; transcellular; transcytosis; vascular wound; repair; hair; smooth muscle; cardlovascular; arteriosclerotic; fibrotic disorder; cellular proliferation; rheumatoid arthritis; diabetes; cirrhosis; tumour; inflammation; neurodegeneration; periodontal; spermatogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to novel inhibitors of cyclin-dependent kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fusion and chimaeric proteins including cyclin-dependent kinase binding motif - used for regulation of cell proliferation and differentiation, for treatment of, e.g. vascular injury, cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1554; DB 20; 99.7%; Pred. No. 2.5e-121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 2; Page 26-27; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamphere L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibrosis and neurodegeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-US15759.
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HIV-1 VP22 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beach DH, Gyuris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-153770/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MITO-) MITOTIX INC
                                                                                                                                                                                                                                                                                                                      tachycardia; HIV-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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The present invention describes a method of identifying the co-activator
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papillomavirus; PV; infection; cell proliferation; E2; peptidomimetic; E1; antiviral; virucide; cytostatic; antiproliferative; dermatological; preneoplastic lesion; neoplastic lesion; cutaneous lesion; wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             which competitively inhibits interaction of a papillomavirus (PV) E2 protein with a PV E1 protein for treating a cell infected with PV or a mammal with a PV-induced condition. (A) has antiviral, virucide, cytostatic, antiproliferative and dermatological activities. Methods from the present invention can be used to treat PV-induced conditions including growth of PV preneoplastic and neoplastic lesions, cutaneous lesions chosen from warts and other benign cutaneous lesions, plantar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of papillomavirus E2 protein peptidomimetics for treating papillomavirus-infected cells and papillomavirus-induced conditions in mammals by inhibiting E1-E2 interaction
                                            common warts, flat warts, genital warts (condyloma acuminatum) and epidermodysplasia verruciformis, laryngeal, oral, pharyngeal, oesophageal and other upper airway papilloma or vaginal, cervical, vulvar, penile and anorectal carcinoma. The EZ inhibitors may also be used to treat epithelial and internal fibropapillomas in animals. The present sequence represents a peptide sequence used in the exemplification of the present invention.
                                                                                                                                                                                                                                                          DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPAGSGGAGRTPTTAPR 120
                                                                                                                                                                                                                                    IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV 300
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                                                                                                                                                               APPINPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         warts (verruca plantaris), common warts (verruca plana), Butcher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes the use of a small organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermodysplasia verruciformis; anorectal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 42; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY79877 standard; Peptide; 301 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Herpes simplex virus type 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-171001/15.
N-PSDB; AAZ88468.
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ID AAY7

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                                                                                                                                                                                                                                                                                              APPNPDAPWTPRVAGENKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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                                                                                                                                                 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR 120
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying co-activator domain specific transcriptional activators contacting a target domain of a selected transcription factor with a peptide display library, where the identified binding peptides are
                                                                                              1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
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   Length 301;
                                        Indels
Score 1554; DB 21;
Pred. No. 2.5e-121;
                                      Mismatches
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INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB60910 standard; Protein; 301 AA.
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 99.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-273380/28.
N-PSDB; AAF58996.
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                     Similarity
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                                    300;
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domain of specific synthetic activators, involving contacting the target domain of a selected transcription factor with a peptide display library, and identifying those sequences which bind to the target domain. In particular, those which bind to the KIX domain of P300/CBP are useful. The peptides can be used in the treatment of diseases related to aberrant KIX-dependent gene transcription, including erythrocythaemia, polycythaemia, haemoglobinopathies, to regulate cell differentiation, to treat neurological diseases, immunological diseases, diabetes, ulcers, skin diseases and cancer, and to aid wound healing. The present sequence is a protein described in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquitin dependent proteolysis modulation; cdc4 phospho design motif; CDP motif; cytostatic; nootropic; antiproliferative; cell proliferation; growth; differentiation; cancer; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              240
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                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                            Score 1554; DB 22;
Pred. No. 2.5e-121;
0; Mismatches 1;
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                                                                                                                                                                                              Query Match 99.6%;
Best Local Similarity 99.7%;
Matches 300; Conservative
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2001US-263774P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       spinal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 125
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                                                                                                                                                                   301 AA;
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24-JAN-2001;
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that targets molecules for ubquitin dependent proteolysis. (C) have cytostatic, nootropic and antiprollferative activity. Also described is a method for the treatment of a disease or condition where affected cells have a defective protein, comprising administering (C) to promote degradation of the target protein in cells by ubiquitin dependent proteolysis. (C) can also be used for modulating the prollferation, growth and/or differentiation of cells. (C) can be used to modulate ubiquitin dependent proteolysis or cell prollferation, growth and or differentiation of cells. (C) is useful in the treatment of cancers and neurodegenerative disorders as well as spinal degeneration. The present sequence represents the HSV-1 VP22 protein which is given in the exemplification of the present invention.
                                                                                                                                                                             The present invention describes a cdc4 phospho design (CPD) mot1f, (C),
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                                                                                   New Cdc4 Phospho Design motif that targets molecules for ubiquitin dependent proteolysis, is useful for the modulation of cell proliferation i.e. cancer treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSV; tegument protein; VP22; UL49; antiviral agent; treatment; cold sore; genital herpes; chickenpox; shingles.
                                                                                                                                                                                                                                                                                                                                                                                                                Length 301;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                              99.6%; Score 1554; DB 23;
llarity 99.7%; Pred. No. 2.5e-121;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus tegument protein VP22.
             Tyers M;
                                                                                                                                                Disclosure; Page 30; 83pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW47194 standard; Protein; 301 AA.
             Tang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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                                        WPI; 2002-164074/21.
N-PSDB; ABA93386.
             Pawson T,
                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 300; Conserv
                                                                                                                                                                                                                                                                                                                                                                                    301 AA;
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             Nash P,
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Herpes simplex virus-1
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                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                         1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60
                                                                                                             New antiviral agent disrupting binding of VP22 to VP16 or gB -
useful for treating infections caused by herpes simplex, e.g. cold
sores and chicken-pox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ubiquitin ligase; SCF; F-box protein; targeted degradation; destabilisation; proteolysis; drug discovery; gene therapy; cancer; oncoprotein; Huntington's disease; gene knockout; delivery systems.
                                                                                                                                                                       tegument protein VP22. VP22 was used in the preparation of a novel antiviral agent, which inhibits the maturation and/or replication of HSV by disrupting association between VP22 and VP16 and/or gB. The agent can be used to treat, e.g. cold sores, genital herpes,
                                                                                                                                                                                                                                                                                                                                                                         APRIQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST
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                                                                                                                                                                                                                                         Length 301;
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                                                                                                                                                                present sequence is the herpes simplex virus (HSV)
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                                                                                                                                                                                                                                         Score 1553; DB 19;
Pred. No. 3e-121;
                                                                      Rixon HWM;
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                                                                                                                                                                                                                                                          Mismatches
                                                                      McLaughlan J,
                                                                                                                                                Example; Pages 49-50; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY83261 standard; Protein; 301
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                      .97WO-GB02036
                                       96GB-0015726
                                                      (MEDI-) MEDICAL RES COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.7
Matches 300; Conservative
                                                                                                                                                                                                        chickenpox and shingles
                                                                      McGeoch DJ,
                                                                                      WPI; 1998-130696/12.
N-PSDB; AAV17085.
                                                                                                                                                                                                                        301 AA;
                      28-JUL-1997;
                                       26-JUL-1996;
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      05-FEB-1998.
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                                                                      Hope RG,
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The F-box proteins are a family of ubiquitin ligases (SCF ubiquitin ligases) which can be used for the targetted degradation of a target polypeptide in vivo. Targetted degradation is achieved by expressing the ubiquitin ligase in a cell linked to the interaction domain of the target polypeptide and thereby recruiting the target polypeptide contensing the layers. Such methods are useful for decreasing or increasing the level of a target polypeptide and for creating and expressing a destabilized polypeptide which is subjected to SCF mediated proteolysis. Degrading any desired protein in a cell is mediated proteolysis. Degrading any desired protein in a cell is useful for preventing or traating diseases caused by the presence of abnormal amount of the specific polypeptides, for drug discovery and for gene therapy. Diseases treated include cancer, by degradation of concoproteins, Huntington's disease, other proliferative disorders and microbial infections. The method provides a quick and easy alternative to gene knockout technology. The target polypeptide can be degraded at all stages, or a specific stage, of development in the contine animal. The hybrid ubiquitin ligase may also include an optional localisation sequence such as this HSV-1 V22 sequence.
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with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Targeting degradation of polypeptide useful for treating cancer and other proliferative disorders, involves conjugating polypeptide with ubiquitin protein ligase or inhibiting ubiquitination using organic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY
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Pred. No. 3e-121;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 99.7%;
Matches 300; Conservative
                                                                                                                         99WO-US23705
                                                                                                                                                                                                                                                        (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                  2000-317970/27
                                                                                                                                                                                                                                                                                                                        Howley P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAZ93717
WO200022110-A2
                                                                                                                         08-OCT-1999;
                                                                                                                                                                                         09-OCT-1998;
                                                            20-APR-2000
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The HSV-1 VP22 polypeptide can be fused to a retinoblastoma (Rb)
inactivator protein sequence to aid targeting and internalization.
The invention concerns methods and reagents for extending the life-span,
e.g. the number of mitotic divisions, of a cell. The method relies on
activation of a telomerase activity and inhibition of one or both of a
activation of a telomerase activity and inhibition of Rb by
cyclin-dependent kinases. Cdk4 and inhibition of Rb by
cyclin-dependent kinases. Cdk4 and inhibits wing reversibly inactivate an
arrest. Rb inactivators can selectively and results in growth
arrest. Rb inactivators can selectively and reversibly inactivate an
cRb/INK4 pathway, especially an Rb/p161NK4a pathway. The oncoprotein MDM2
cc and can also be used in the methods. Other molecules which can be used
include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which
differs from at one or more of residues K22, R24, H95 and/or D97.
Additional constructs include a papilloma virus E7 protein, or other
cviral oncoprotein which bypasses Rb and/or p53. Antisense constructs of
the Rb and p161NK4a genes may also be used. The methods are useful for
increasing the proliferative capacity of cells. The cells are
cubesquently of use in pharmaceutical and cosmetic preparations used to
treat conditions related to (premature) ageing, e.g. macular degeneration
and arretrosoclearosis. The cells can also be used to replace tumour cell
clines in vitro and for studies on biochemical and physiological aspects
of growth and differentiation. Long lived (immortal) cells could also be
constructs of the colls.
Collines in the moderation of normal or genetically engineered
                                                                                                                                                                                                           hEST2; telomerase; catalytic subunit; reverse transcriptase; life-span, retinoblastoma; p53; tumour suppressor; inhibitor; arteriosclerosis; proliferation; immortal; tumour therapy; macular degeneration; activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method for increasing the proliferative capacity of cell lines comprises administering agents reversibly activating telomerase activity and reversibly inactivating Rb/INK4 and/or. p53 pathways useful in treating age related diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 31-32; 123pp; English.
                                         AAY96574 standard; Protein; 297 AA
                                                                                                                                                                                                                                                                          INK4; HSV-1; VP22; fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0109891.
99US-0120549.
                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                 Herpes simplex virus 1.
                                                                                                                                                               HSV-1 VP22 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hannon GJ, Beach DH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENETICA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-400055/34.
N-PSDB; AAA29395.
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                                                                                                                        12-SEP-2000
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                                                                              AAY96574;
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RESULT 1
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Gaps

Length 297; Indels 4

97.4%; Score 1520; DB 21; 98.3%; Pred. No. 1.6e-118; iive 0; Mismatches 1;

Query Match 97.4 Best Local Similarity 98.3 Matches 296; Conservative

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DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPAGSGGAGRTPTTAPR 120
                117 APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLÄRKLHFST 176
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                                                           APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAQGLARKLHFST
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                                                                                                                  APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
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GenCore version $5.1.4_p5_4578$ Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

May 21, 2003, 17:33:24 ; Search time 25.7613 Seconds Run on:

(without alignments)
343.784 Million cell updates/sec

US-09-522-278B-12 1561 1 MTSRRSVKSGPREVPRDEYE......PTERPRAPARSASRPRRPVE 301 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

262574 segs, 29422922 residues Searched:

262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100%. Listing first 45 summaries

Database :

Issued_patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 21, Appl	'n	Sequence 12, Appl	7	2	e,	18,	19	2, 4	20	14,	99	99	2, 4	14,	Sequence 2, Appli	26,	26,	40,	40,	41,	41,	3, A	Sequence 14, Appl	14,	14,	Sequence 2, Appli
	, QI	US-08-303-861-21	US-09-011-073A-1	US-09-347-504-12	US-09-230-421-2	US-09-336-093-5	US-09-230-421-3	US-08-303-861-18	US-08-303-861-19	US-09-213-343-2	US-08-303-861-20	US-09-347-504-14	US-08-680-726A-66	US-09-092-409-66	US-09-011-073A-2	US-09-230-421-14	PCT-US91-06532-2	US-08-483-533-26	US-09-283-471A-26	US-08-483-533-40	US-09-283-471A-40	US-08-483-533-41	US-09-283-471A-41	PCT-US91-06532-3	US-08-795-868-14	US-09-303-069-14	-09	US-09-082-737-2
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	Match Length	301	301	301	301	246	.144	258	258	258	302	37	139	139	34	32	263	258	258	264	264	355	355	355	661	199	661	591
8	Match	100.0	100.0	9.66	99.3	77.1	36.7	17.4	17.4	17.4	14.4	11.5	11.1	11.1	10.8	10.6	9.1	0.6	0.6	9.0	9.0	8.7	8.7	8.7	8.4	8.4	8.4	8.4
	Score	1561	1561	1554	1548	1203.5	573	271.5	271.5	271.5	225.5	179	172.5	172.5	169	166	142.5	141	141	141	141	136.5	136.5	136.5	131.5	131.5	131.5	130.5
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-	Sequence 4	Sequence 45- Appl	Sequence 78, Appl	Sequence 8, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 369, App	Sequence 14, Appl	Sequence 84, Appl	Sequence 74, Appl	Sequence 58, Appl	104,	Sequence 44, Appl	Sequence 42, Appl	Sequence 142, App	Sequence 50, Appl	Sequence 46, Appl	
	US-08-483-533-43	US-09-283-471A-43	US-09-413-814-78	US-09-232-468A-8	US-08-690-473-2	US-09-259-821A-2	US-08-843-659-2	US-09-199-637A-369	US-07-757-022B-14	US-07-757-022B-84	US-07-757-022B-74	US-07-757-022B-58	US-07-757-022B-104	US-07-757-022B-44	US-07-757-022B-42	US-07-757-022B-142	US-07-757-022B-50	US-07-757-022B-46	
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	252	252	882	404	1298	1298	1298	265	941	1022	1038	1049	1140	1270	1311	1313	1314	1320	
	8.3	8.3	8.2	8.2	8.1	8.1	8.1	7.8	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	7.7	
	129.5	129.5	128	127.5	126.5	126.5	126.5	122	120.5	120.5	120.5	120.5	120.5	120.5	120.5	120.5	120.5	120.5	
	28	29	. 30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5	

ALIGNMENTS

RESULT 1 US-08-303-861-21 ; Sequence 21, A	861-21 21, Application US/08303861
; Patent No.	atent No. 6086902 GENERAL INFORMATION:
; APPLICANT:	_
; APPLICANT:	CANT: LIANG, XIAOPING CANT: BABIUK, LORNE A.
; TITLE	WENTION:
; TITLE	OF.
CORRESI	OF SECUENCES:
, ADD!	٠,
STRI	<u></u>
STATE	CITY: PAIO ALCO
COOL	COUNTRY: USA
; ZIP	ZIP: 94304-1018
COMPU	COMPUTER READABLE FORM:
MED	MEDIUM TYPE: Floppy alsk
OPE	COMPUTER: IDM PC COMPACIDIE OPERATING SYSTEM: PC-DOS/MS-DOS
SOF	SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRE	CURRENT APPLICATION DATA:
, APPI	N NOIL
11.4 14.15	FILING DATE: UM-SEP-1994
ATTOR	ATTORNEY / AGENT INFORMATION:
, NAME:	E: PARK, FREDDIE K.
REG	RATION
; REF	REFERENCE/DOCKET NUMBER: 29310-20020.20
; TELEC	TELECOMMUNICATION INFORMATION:
; TEL	EPHONE: (415) 813-5600
TEL	TELEFAX: (415) 494-0792
TABODAA	INDIANT ON EACH TO NO. 21.
SEOTE	SECTION OF THE PROPERTY OF THE
LENC	LENGTH: 301 amino acids
; TYPE:	amino
; STR	ESS
; TOPC	TOPOLOGY: linear
US-08-303-861-21	361-21
Query Match	100.0%; Score
Best Local Matches 30	Similarity 11; Conservat
,00	MTSRSVKSGPREVPRDEVEDLYVTPSSGMASPDSPDDTSRRGALOTRSRORGEVREVOV 60
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Db 1 N	MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQRGEVRFVQY 60

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SOFTWARE:
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121 APRTORVATKAPAAPAAETTRGRKSAOPESAALPDAPASTAPTRSKTPAOGLARKLHFST 180
                                                                                                                        181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT 240
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                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: O'Hare et al.
TITLE OF INVENTION: TRANSPORT PROFEINS AND THEIR USES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Klarquist Sparkman Campbell Leigh
ADDRESSEE: Whinston, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,073A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CB96/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: United States of America ZIP: 97204-2988
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/09011073A Patent No. 6184038 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: One World Trade Center
STREET: 121 S.W. Salmon Street
STREET: Suite 1600
CITY: Portland
STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Earp, David J.
REGISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (503) 226-7391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (503) 228-9446
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        US-09-011-073A-1
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61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPQRARAPPPAGSGGAGRTPTTAPR 120
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                                               DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPPAGSGGAGRTPTTAPR
                                                                                                                                           APRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAAPASTAPTRSKTPAQGLARKLHFST
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REFERENCE: HMV-041.01
CURRENT APPLICATION NUMBER: US/09/347,504
CURRENT FILLING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 99.6%; Score 1554; DB 4; Best Local Similarity 99.7%; Pred. No. 6.2e-127; Matches 300; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: HSV-1 VP22 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/09347504 Patent No. 6399075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Howley, Peter M. APPLICANT: Benson, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: HOWLEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: HSV
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LENGTH: 301
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Patent No. 6348185
GENERAL INFORMATION:
APPLICANT: Washington University School of Medicine
TITLE OF INVENTION: MEMBRANE-PERMEANT PEPTIDE COMPLEXES FOR MEDICAL
TITLE OF INVENTION: IMAGING, DIAGNOSTICS, AND PHARMACEUTICAL THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRORGEVRFVQY
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                                                                                                                                                                                                                                                                                                  Length 301;
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                                             GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: ANTI-HEREFOREVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P18189C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4;
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Pred. No. 2.1e-126;
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Pred. No. 1e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/336,093A CURRENT FILING DATE: 1999-06-18 NUMBER OF SEQ ID NOS: 31 SOFTWARE PALENTIN VET. 2.1 SEQ ID NO 5
                                                                                                                                                                              FastSEQ for Windows Version 3.0
                                                                                                                            CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 3.(
SEQ ID NO 2
                 Sequence 2, Application US/09230421
Patent No. 6200577
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80.78;
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llarity 99.3%;
Conservative
                                                                                                                                                                                                                                               ; ORGANISM: HERPESVIRUS TYPE US-09-230-421-2
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Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                Similarity
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US-09-336-093-5
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US-09-230-421-2
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Matches
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121 APRTORVATKAPAAPAAETTRGRKSAQPESAALPDAPASTAPTRSKTPAOGLARKLHFST 180
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 ASTAPTRSKTPAGGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAA 81
                                                                                                                                                            181 APPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLGITT
                                                                                                                                                                                                                                                                                     241 IRVTVCEGKNLLQRANELVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASRPRRPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 144;
                                                                     61 DESDYALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGPARAPPPAGSGGAGR'
                  GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: LIANG, XIAOPING
APPLICANT: BABLIK, LORNE A.
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE :
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
MTSRRSVKSGPREVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQTRSRQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Medical Research Council
TITLE OF INVENTION: ANTI-HERPESVIRAL ALENTS AND ASSAYS
TITLE OF INVENTION: THERPEOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/230,421
CURRENT FILING DATE: 1999-01-25
NUMBER OF SEO ID NOS: 14
SOFTWARE: PASTSEO FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 18, Application US/08303861 Patent No. 6086902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09230421 Patent No. 6200577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 36.7
Best Local Similarity 100.
Matches 110; Conservative
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100 RAPPPPAGSG-----GAGRT---PTTAPRAPRTQRVATKAPAAPA-----AETTRGRKSA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 QPESAALPDAPASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207 RLAAMHARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQD 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 17.4%; Score 271.5; DB 3; Best Local Similarity 31.2%; Pred. No. 4.4e-16; Matches 81; Conservative 25; Mismatches 109;
                                                                                            Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                     29310-20020.20
                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENTIN Release #1.0, Ve CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,861 FILING DATE: 09-SEP-1994
CLASSIFICATION: 435
                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 293
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEO ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
STRANDEDNESS: single
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; ORGANISM: Bovine herpesvirus 1
US-09-213-343-2
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TELEFAX: (415) 494-0792
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  COMPUTER READABLE FORM:
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US-08-303-861-19
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LENGTH: 258
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APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: LIANG, LORNE A
TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE
TITLE OF INVENTION: VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                          OPPERATION SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/303,861 FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.4%; Score 271.5; DB 3;
31.2%; Pred. No. 4.4e-16;
tive 25; Mismatches 109;
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ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08303861
Patent No. 6086902
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 2931(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 VDAATATRGRSAASRPTERP 286
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amino acid
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Best Local Similarity 31.2%
Matches 81; Conservative
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MOLECULE TYPE: protein

US-08-303-861-18
                                              California
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                                                                                     94304-1018
                     Palo Alto
                                                                                                                                                                                                                                                                             FILING DATE: 05 CLASSIFICATION:
                                                                      USA
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US-08-303-861-19
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STATE: Ca
COUNTRY:
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Gaps

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Length 258;

Gaps 45; Length 258; Indels Sequence 2, Application US/09213343
Patent No. 6316252
GENERAL INFORMATION:
APPLICANT: Harms, Jarome S.
APPLICANT: Splitter, Gary A.
TITLE OF INVENTION: Biotherapeutic Delivery System:
FILE REFERENCE: 960296.99564
CURRENT APPLICATION NUMBER: US/09/213,343
CURRENT PAPLICATION NUMBER: 1998-12-17
NUMBER OF SEQ ID NOS: 4 17.4%; Score 271.5; DB 4; 31.2%; Pred. No. 4.4e-16; Live 25; Mismatches 109; 81; Conservative Best Local Similarity Matches 81; Conserve

94304-1018

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---VKPK---LEDSP-K 141
                                                                                                                                                           160 TAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQ 219
                                                                                                                                                                                                  142 RAPPGAGAIASG--RPISFSTAPKTATSSWCGPTPSYNKRVFCEAVRRVAAMQAQKAAEA 199
                                                                                                                                                                                                                                                                            100 RAPPPPAGSGGAGRTPTTAPRAPRTQRVATKAPAAPAAETTRGRKSAQPESAALPDAPAS 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTHER INFORMATION: Description of Artificial Sequence: VP22 OTHER INFORMATION: (C-terminal domain) peptide US-09-347-504-14
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Pred. No. 3.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kasukawa, Hiroaki
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: PAPILLOMAVIRUS-INFECTED CELLS
FILE REPERBANCE: HMV-041.01
CURRENT FILING DATE: 1999-07-02
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PALENTIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      258 -- LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
                                                                                                                                                                                                                                                                                                                                                                                  260 GGMGNEPMYAQVRKPKSRTDTQTTGRITNRSR--ARSASR 297
                                                                                                                                                                                                                                                220 LWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANE-----
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                                                                                                               ----SRSFTKNAA-----
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1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-680-726A-66; Sequence 66, Application US/08680726A; Patent No. 5804197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/09347504 Patent No. 6399075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.5%; Scor.
100.0%; Pre
0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Howley, Peter M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 36; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Howley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Benson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
STREET: 17
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US-09-347-504-14
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                                                                                     100 RAPPPPAGSG-----GAGRT---PTTAPRAPRTQRVATKAPAAPA----AETTRGRKSA 146
                                                                                                                                 63 AAAVQPAARGRDRAAAAGTTVAAPAAPARRSSSRASSRPPRAAADPPVLRPATRGSSGG 122
                                                                                                                                                                               QPESAALPDAPASTAPTRSKTPAQGLARKLHFSTAPPNPDAPWTPRVAGFNKRVFCAAVG 206
                                                                                                                                                                                                                       123 AGAVAVGP--PRPRAPPGANAVASG--RPLAFSAAPKTPKAPWCGPTHAYNRTIFCEAVA 178
                                                                                                                                                                                                                                                                   RLAAMHARMAAVQLWDMSRPRTDEDLNELLGITTIRVTVCEGKNLLQRANELVNPDVVQD: 266
                                                                                                                                                                                                                                                                                                 ---A 99
                                           10 DEDDYEYSDLWVRENSLYDYESGSDDHVYEELR-----AATSGPEPSGRRASVRACAS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- REVPRDEYEDLYYTPSSGMASPDSPPDTSRRGALQ 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 TRSRORGEVRFVQYDESDYALYGGSSSEDDEHPEVPRTRRP-----VSGAVLSGPGPA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 TARRSVVVGPPDDSDDSLGYITTVGADSPSPVYADLYFEHKNTTPRVHQPNDSS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RECOMBINANT BOVINE HERPESVIRUS TYPE VACCINES
  ----ALYGGSSSEDDEHPEVPRTRRPVSGAVLSGPGP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%; Score 225.5; DB 3; 26.2%; Pred. No. 5.2e-12; ive 27; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/303,861
FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/08303861
Patent No. 6086902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: ZAMB, TIMOTHY
APPLICANT: LIANG, XIAOPING
APPLICANT: BABIUK, LORNE
TITLE OF INVENTION: RECOMBINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 29
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           267 VDAATATRGRSAASRPTERP 286
                                                                                                                                                                                                                                                                                                                                                                                                     239 AARGSTSGGESRLRGERARP 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : MORRISON & FOER
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 755 Page N
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: SIR
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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61 DESDY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-303-861-20
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90 KAVIRITISECLGILKTANTPFSCGOKTADDV-----KFKSHSSR-----RSKSOSRSR 128
                                                                                                                                                                                                                                 178. FSTAPPNPDAPWTPRVAGFNKRVFCAAVGRLAAMHARMAAVQLWDMSRPRTDEDLNELLG 237
                                                                                                                                                                                                                                                                                                                 238 ITTIRVTVCEGKNLLQRANE--LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                   Length 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: O'Hare et al.
TITLE OF INVENTION: TRANSPORT PROTEINS AND THEIR USES NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Klarquist Sparkman Campbell Leigh & ADDRESSEE: Whinston, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 169; DB 4; I
Pred. No. 2.4e-08;
                                                                                                                                                                      .4e-08;
                                                                                                                                               11.1%; Score 172.5;
35.0%; Pred. No. 7.4e
tive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Earp, David J.
RECISTRATION NUMBER: 41,401
REFERENCE/DOCKET NUMBER: 5759-49294/DJE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 97204-2988
COMPUTER READABLE FORM:
MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 7.0 & ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/011,073A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB96/01831
FILING DATE: JULY 25, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United States of America ZIP: 97204-2988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: One World Trade Center STREET: 121 S.W. Salmon Street STREET: Suite 1600 CITY: Portland STATE: Oregon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09011073A Patent No. 6184038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.8%; SCC
100.0%; Pre
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                       : 139 amino acids
amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          Conservative
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Best Local Similarity 100.
Matches 34; Conservative
      SEQUENCE CHARACTERISTICS
                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
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Best Local Similarity
Matches 43; Conserva
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                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           129 HSR 131
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US-09-011-073A-2
                                                                                                          US-09-092-409-66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   238 ITTIRVTVCEGKNLLQRANE--LVNPDVVQDVDAATATRGRSAASRPTERPRAPARSASR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 FSNTPKTPKFPWYGATHLYNKNVFCEAVRRCASKHAIEAASSIWDLNPPQSNEELEKFLT 79
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: FECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                        .4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%; Score 172.5;
35.0%; Pred. No. 7.4¢
tive 20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 2618-46-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                       APPLICATION NUMBER: US/08/680,726A
FILING DATE: 12-JUL-1996
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/092,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAPTUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/680,726
FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 66, Application US/09092409 Patent No. 6159478
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGIEVRATION UNDRER: 32,020
REFERENCE/DOCKET NUMBER: 2618
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-0723
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Connell, Gary J
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 66:
                                                                                                                                                                                                                                                                                         : 139 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 35.0%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-680-726A-66
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colorado: U.S.A.
                                                                 FILING DATE: 12
CLASSIFICATION:
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CITY: Denver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Colo
COUNTRY: U.
ZIP: 80203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
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US-09-092-409-66
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Search completed: May 21, 2003, 17:38:37 Job time: 26.7613 secs

Gaps

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Ouery Match
10.6%; Score 166; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 32; Conservative 0; Mismatches 0; Indels

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